

forth the rules, upon allowance of product claims, for rejoinder of process claims covering the same scope of products.

Applicants have canceled claims 9-12, 15-24, and 26.

Support for the amendments to claim 1 is found in claim 1 as originally filed and in the specification at page 1, lines 32-33; at page 2, lines 1-3; and at page 5, lines 23-24.

Support for the amendments to claim 4 is found in claim 4 as originally filed and in the specification at page 1, lines 32-33; at page 2, lines 1-3; and at page 5, lines 23-24.

Support for the amendments to claim 13 is found in claim 13 as originally filed and in the specification at page 3, lines 4-7; at page 40, lines 28-30; and on the first page of Figure 2, at line SEQ ID NO: 15, G896.

Claims 14 and 25 have been amended in response to the Examiner's objections.

Claim 27 has been amended to place the claim in proper dependent form: support for the amendment can be found in the specification at page 28, lines 3-16; at page 36, lines 13-33 and continued on pages 37-40; and in Figure 2, at SEQ ID NO: 15.

Response to Examiner's Detailed Action

1. At page 2, first paragraph of the Examiner's Office action (Paper No. 11, mailed 07/30/2002), the Examiner has inadvertently introduced a typographical error into the Office action when referring to "SEQ ID NO:15(G986)". Applicants disclosed in Figure 1, column 2 (GID), that SEQ ID NO:15 refers to Mendel internal code reference number G896, not G986.

6. Applicants have submitted corrected Figure 1 and corrected Figure 2 as formal drawings to conform to the draftsperson's objections and comments. No new matter is introduced by such corrected figures and entry of the corrected Figure 1 and Figure 2 is respectfully requested.

7. Applicants respectfully submit that an appendix (Appendix A) was submitted at the time of filing the instant application. Applicants have herewith included a copy of the Patent Application Transmittal Form which clearly shows that a set of CD-ROMs were submitted as an Appendix (see Box 7 of Application Elements) (Exhibit 1).

8. Applicants have amended the specification to remove text which could be identified as an

embedded hyperlink and/or other form of browser-executable code. Applicants submit that the replacement text cannot be identified as an embedded hyperlink and/or other form of browser-executable code. Applicants believe no new matter has been introduced by this amendment.

Claim Objections

The Examiner has objected to claims 1-8, 13, 14, 25 and 26 because of the following informalities: the Examiner stated that the claims are directed to non-elected SEQ ID NOs, and should be amended to remove any reference to non-elected inventions and that appropriate correction is required.

The Examiner suggested that at claim 14, the phrase "a polynucleotide of claim 4" should read -- "the polynucleotide of claim 4" -- because claim 4 is directed to an isolated or recombinant polynucleotide in the singular.

The Examiner suggested that at claim 25, the phrase "an isolated or recombinant polynucleotide of claim 4" should read -- "the polynucleotide of claim 4" -- because claim 4 is directed to an isolated or recombinant polynucleotide in the singular.

The Examiner suggested that at claim 26, the phrase "an isolated or recombinant polypeptide of claim 11" should read -- "the isolated or recombinant polypeptide of claim 11" -- because claim 11 is directed to an isolated or recombinant polypeptide in the singular. The Examiner stated that, in addition, claim 26 is directed to a non-elected invention.

The Examiner stated that claim 26 is objected to under 37 C.F.R. § 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. The Examiner stated that Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. The Examiner stated that claim 26 is directed to a "plant" whereas claim 11 is directed to "an isolated or recombinant polypeptide", hence claim 26 fails to further limit the polypeptide of claim 11.

In response, Applicants have canceled claim 26.

Applicants have amended claims 1 and 4 to remove any reference to non-elected inventions. Applicants have amended claims 14 and 25 as suggested by the Examiner.

Applicants therefore respectfully request that the Examiner withdraw the objections to claims 1-8, 13, 14, and 25.

Rejection of Claims 1-8, 13, 14, 25 and 26 under 35 U.S.C. § 112, second paragraph

The Examiner rejected claims 1-8, 13, 14, 25, and 26 under 35 U. S. C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner stated that claims 1 and 4 are indefinite because said claims refer to an "Appendix A" which does not appear in the specification, hence it is unclear what the metes and bounds of the claims are.

The Examiner stated that at claims 1 (a) and 4(a), the phrase "comprising a sequence selected from" is indefinite because it is unclear if Applicant is referring to the nucleotide sequence or the polypeptide, in view of the lack of an "Appending A" in the specification.

The Examiner stated that at claims 1(b) and 4(b), the phrase "comprising a conservative substituted variant of a polypeptide of (a)" because it is unclear how the polypeptide of (a) would also comprise a polypeptide comprising a conservative substituted variant. The Examiner stated that it is unclear if Applicant is claiming a fusion polypeptide or a variant of the polypeptide of (a) comprising a conservatively substituted amino acid sequence and that appropriate correction is required.

The Examiner stated that at claims 1 (d) and 4(d), the phrase "a nucleotide sequence of (c)" is indefinite and should read -- the nucleotide sequence of (c) --. The Examiner also suggested that Applicants see 1 (e, h, and i) and 4 (e, h, and i) for similar issues.

The Examiner stated that at claims 1(e) and 4(e), the phrase "hybridizes under stringent conditions" is indefinite because it is unclear what the metes and bounds of this limitation are. The Examiner stated that Applicant's definition on page 12, 1st paragraph, of the specification does not teach what time limits are used to produce said "stringent conditions".

The Examiner stated that at claims 1 (g) and 4(g), the limitation "any of (a)-(f)", renders the claims indefinite because it is unclear what the metes and bounds of the claims are.

The Examiner stated that at claims 1(l) and 4(l), the phrase "a conserved domain" is indefinite because the phrase is relative and does not state the metes and bounds of the claimed invention. The Examiner stated that Figure 1 teaches Applicant's interpretation of the conserved domain encoded by SEQ ID NO: 15, hence the claim should read -- the conserved domain encoded by a polynucleotide having the nucleotide sequence of SEQ ID NO: 15 --.

The Examiner stated that claim 13 is indefinite and generally narrative, said claim being directed to a method for producing a plant, but "altering" does not denote a positive method step by which one would practice the claimed method. The Examiner stated that the limitation "altering" does not state the metes and bounds of the claimed method. In addition, the Examiner continued, claim 13 is dependent upon a claim directed to the non-elected invention of claim 11, and should be amended accordingly.

The Examiner stated that at claim 26, it is unclear if the plant comprises "the activity of" an isolated or recombinant polypeptide or if the plant comprises [altered activity of] an isolated or recombinant polypeptide. Hence, the Examiner stated, it is unclear what the metes and bounds of the claimed invention are.

Applicants have cancelled claim 26. Applicants have amended claim 1 to recite: "A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:110; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of SEQ ID NO:110; (c) a nucleotide sequence comprising SEQ ID NO:15; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and (f) a nucleotide sequence comprising the complementary nucleotide sequence of a nucleotide sequence of (a), (b), (c), (d), or (e)".

Applicants have amended claim 4 to recite: "An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:110; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of SEQ ID NO:110; (c) a nucleotide sequence comprising SEQ ID NO:15; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and (f) a nucleotide sequence comprising the complementary nucleotide sequence of a nucleotide sequence of (a), (b), (c), (d), or (e)".

Applicants have amended claim 13 to recite: "A method for producing a modified plant having a modified trait, the method comprising: (i) transforming a plant with the isolated or recombinant polynucleotide of claim 4, thereby producing a modified plant, and (ii) selecting the modified plant for a modified trait thereby providing the modified plant with a modified trait, wherein the trait so modified is that of increased resistance to fungal pathogens".

Applicants have removed recitation to "fragment" and "at least 15 consecutive nucleotides of SEQ ID NO:15" in claims 1 and 4.

With regard to the Examiner's concern that a "time limit" is necessary to define "stringent conditions", on Page 11, lines 29-34, and page 12, lines 1-11, of the specification. Applicants note that the

factors that can influence the degree of stringency are disclosed.

The specification, at page 9, lines 27-34, recite hybridization and wash conditions are disclosed as being in references cited earlier in the application in which time limits for incubating polynucleotides under stringent conditions are described. Specifically, the teachings of Sambrook et al. (incorporated by reference in the application in its entirety) are disclosed on page 9 of the specification ("Procedures for identifying and isolating DNA") wherein pages 9.47-9.55 of Sambrook et al. teach such art-recognized times for hybridization under stringent conditions (copy of cited teachings submitted herewith as Exhibit 2). Thus, the "metes and bounds" of the hybridization steps would be understood by one skilled in the art.

As is recognized in the art, the most critical aspects of hybridization and wash steps are ionic strength and temperature parameters. Given the range of conditions an experimenter may wish to impose on a hybridization protocol (within the ranges disclosed in the specification), in each case hybridizing polynucleotide molecules reach full equilibration in the stringent chemical environment and temperature in a relatively short time, and disassociation and elution of molecular species requires even less. The skilled artisan knows that these periods are generally on the order of hours for the former and minutes for the latter (see, for example, Sambrook). For all of these reasons it would be trivial for a given experimenter skilled in the art of routine hybridization studies to determine an appropriate time period for successful hybridization and washing given the conditions provided in the specification, particularly given the reference provided and the time parameters taught therein.

Therefore, with the arguments and amendments to claims 1, 4, and 13 set forth above, Applicants respectfully request that the rejection of claims 1-8, 13, 14, and 25 under 35 U.S.C. § 112, second paragraph, be withdrawn.

Rejection of Claims 1-8, 13, 14, 25, and 26 under 35 U.S.C. § 112, first paragraph

The Examiner rejected claims 1-8, 13, 14, 25 and 26 under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The Examiner stated that Applicant claims an isolated or recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising a sequence selected from "Appendix A", comprising a conservative substituted variant of said polypeptide, a nucleotide sequence comprising silent substitutions of said nucleotide sequence, a nucleotide sequence comprising at least 15 consecutive nucleotides of said nucleotide sequence, a nucleotide sequence comprising a subsequence or fragment of

said nucleotide sequence encoding a polypeptide that modifies a plant's trait, having at least 31 % or 60% identity to said nucleotide sequence or encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A. The Examiner stated that Applicant also claims transgenic plants comprising a recombinant polynucleotide comprising said nucleotide sequence, a cloning or expression vector comprising said polynucleotide, and a method of producing a plant having a modified characteristic using said polynucleotide.

The Examiner stated that Applicant describes a polynucleotide having the nucleotide sequence of SEQ ID NO: 15, the elected invention, said polynucleotide having been isolated from *Arabidopsis thaliana* and an *Arabidopsis thaliana* plant having a "knockout" of said polynucleotide exhibiting increased susceptibility to *Fusarium* (see Figure 2). The Examiner stated that it is unclear from Figure 2 and the specification if the term "knockout" is to be interpreted as meaning a plant lacking a polynucleotide or a plant in which expression of said polynucleotide has been suppressed in some way.

The Examiner stated that Applicant does not describe other polynucleotides comprising a conservative substituted variant of a polypeptide shown in Appendix A, a nucleotide sequence comprising silent substitutions of said nucleotide sequence, a nucleotide sequence comprising at least 15 consecutive nucleotides of said nucleotide sequence, a nucleotide sequence comprising a subsequence or fragment of said nucleotide sequence encoding a polypeptide that modifies a plant's trait, having at least 31 % or 60% identity to said nucleotide sequence or encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A". The Examiner stated that Applicant does not describe any unique identifying features of a polynucleotide having the nucleotide sequence of SEQ ID NO: 15, what type of polypeptide is encoded by a polynucleotide having the nucleotide sequence of SEQ ID NO: 15, other than it is a transcription factor, or what "modified trait" a plant comprising a recombinant polypeptide comprising a conservative substituted variant of said polypeptide, a nucleotide sequence comprising silent substitutions of said nucleotide sequence, a nucleotide sequence comprising at least 15 consecutive nucleotides of said nucleotide sequence, a nucleotide sequence comprising a subsequence or fragment of said nucleotide sequence encoding a polypeptide that modifies a plant's trait, having at least 31 % or 60% identity to said nucleotide sequence or encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A would exhibit compared to a wild type plant.

Hence, the Examiner continued, it is unclear from the instant specification that Applicant was in possession of the invention as broadly claimed.

The Examiner stated that, in the instant case, the claimed isolated or recombinant polynucleotide is only described by the function that it encodes a polypeptide that modifies a trait in a plant, and

transgenic plants with a modified trait comprising said polynucleotide. In addition, it is art-recognized that different plant transcription factors regulate different plant traits, and that some plant transcription factors regulate multiple traits. Hence, the Examiner continued, the art recognizes that there is no clear correlation between the structure of a plant transcription factor polynucleotide or the encoded polypeptide and the specific function of the transcription factor, that being the regulation of gene expression in general as opposed to regulating root development, for example.

15. The Examiner stated that claims 1-8, 13, 14, 25 and 26 are rejected under 35 U.S.C. § 112, first paragraph, because the specification, while being enabling for an isolated or recombinant polynucleotide encoding the polypeptide encoded by a polynucleotide having the nucleotide sequence of SEQ ID NO: 15, transgenic plant comprising a knockout of said polynucleotide having reduced resistance to fungal pathogens and methods of making said transgenic plant, does not reasonably provide enablement for any polynucleotide encoding a polypeptide that modifies a plant's trait, any plant comprising said polynucleotide and methods of making same. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The Examiner stated that Applicant claims an isolated or recombinant polynucleotide comprising a nucleotide sequence encoding a polypeptide comprising a sequence selected from "Appendix A", comprising a conservative substituted variant of said polypeptide, a nucleotide sequence comprising silent substitutions of said nucleotide sequence, a nucleotide sequence comprising at least 15 consecutive nucleotides of said nucleotide sequence, a nucleotide sequence comprising a subsequence or fragment of said nucleotide sequence encoding a polypeptide that modifies a plant's trait, having at least 31 % or 60% identity to said nucleotide sequence or encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A. The Examiner stated that Applicant also claims transgenic plants comprising a recombinant polynucleotide comprising said nucleotide sequence, a cloning or expression vector comprising said polynucleotide, and a method of producing a plant having a modified characteristic using said polynucleotide.

The Examiner stated that Applicant teaches a transgenic *Arabidopsis thaliana* "knockout" plant in Figure 2, transformed with a polynucleotide having the nucleotide sequence of SEQ ID NO:15, said plant having increased susceptibility to *Fusarium*.

The Examiner stated that Applicant does not teach other polynucleotides comprising a conservative substituted variant of a polypeptide shown in Appendix A, a nucleotide sequence comprising silent substitutions of said nucleotide sequence, a nucleotide sequence comprising at least 15

consecutive nucleotides of said nucleotide sequence, a nucleotide sequence comprising a subsequence or fragment of said nucleotide sequence encoding a polypeptide that modifies a plant's trait, having at least 31 % or 60% identity to said nucleotide sequence or encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A. The Examiner stated that Applicant does not teach any unique identifying features of a polynucleotide having the nucleotide sequence of SEQ ID NO: 15, what type of polypeptide is encoded by a polynucleotide having the nucleotide sequence of SEQ ID NO: 15, other than it is a transcription factor, or what "modified trait" a plant comprising a recombinant polypeptide comprising a conservative substituted variant of said polypeptide, a nucleotide sequence comprising silent substitutions of said nucleotide sequence, a nucleotide sequence comprising at least 15 consecutive nucleotides of said nucleotide sequence, a nucleotide sequence comprising a subsequence or fragment of said nucleotide sequence encoding a polypeptide that modifies a plant's trait, having at least 31% or 60% identity to said nucleotide sequence or encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A would exhibit compared to a wild type plant. In addition, the Examiner stated, at claim 26, Applicant does not teach altered or altering expression levels of an isolated or recombinant polypeptide in a plant by methods other than overexpression or suppression using a polynucleotide having the sequence of SEQ ID NO: 15.

The Examiner stated that Applicant has provided limited guidance for the claimed invention. The Examiner stated that the specification gives only limited guidance as to what "plant trait" is "modified" in transgenic *Arabidopsis thaliana* plants transformed with the disclosed polynucleotide, specifically a polynucleotide having the nucleotide sequence of SEQ ID NO: 15, of the elected invention. The Examiner stated that Applicant provides no guidance as to what special or specific properties the transcription factor encoded by SEQ ID NO: 15 has that enables said transcription factor to modify a specific plant trait, only that it is a transcription factor. The Examiner stated that Applicant only provides examples directed to transgenic plants transformed with a homologous polynucleotide sequence, applicant does not provide examples of heterologous plants transformed with the disclosed polynucleotide or what plant traits are modified in heterologous plants by the taught transcription factor. The Examiner stated that the art teaches that equivalent or similar biological functions can be controlled by different families of transcription factors and that DNA binding domains that are found in all three eukaryotic kingdoms often control different functions in each one (see Riechmann et al. 2000, *Science* Vol.290, pages 2105-2110, in particular page 2109, left column, last paragraph). Hence, the Examiner concluded, it would have required undue trial and error experimentation by one of skill in the art at the time of Applicant's invention to screen through a myriad of polynucleotides comprising a nucleotide sequence encoding a polypeptide

comprising a conservative substituted variant of a polypeptide shown in Appendix A, a nucleotide sequence comprising silent substitutions of said nucleotide sequence, a nucleotide sequence comprising at least 15 consecutive nucleotides of said nucleotide sequence, a nucleotide sequence comprising a subsequence or fragment of said nucleotide sequence encoding a polypeptide that modifies a plant's trait, having at least 31 % or 60% identity to said nucleotide sequence or encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A, transform a myriad of plants and determine what polynucleotides modify what plant trait as broadly claimed.

The Examiner stated that at claim 26, it would have required undue trial and error experimentation by one of skill in the art at the time of Applicant's invention to identify all method of altering expression levels or altering the activity of the polypeptide encoded by SEQ ID NO: 15.

In response, Applicants have cancelled claim 26. Applicants have amended claim 1 to recite: "A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:110; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of SEQ ID NO:110; (c) a nucleotide sequence comprising SEQ ID NO:15; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and (f) a nucleotide sequence comprising the complementary nucleotide sequence of a nucleotide sequence of (a), (b), (c), (d), or (e)".

Applicants have amended claim 4 to recite: "An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:110; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of SEQ ID NO:110; (c) a nucleotide sequence comprising SEQ ID NO:15; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and (f) a nucleotide sequence comprising the complementary nucleotide sequence of a nucleotide sequence of (a), (b), (c), (d), or (e)".

Applicants have amended claim 13 to recite: "A method for producing a modified plant having a modified trait, the method comprising: (i) transforming a plant with the isolated or recombinant polynucleotide of claim 4, thereby producing a modified plant, and (ii) selecting the modified plant for a

modified trait thereby providing the modified plant with a modified trait, wherein the trait so modified is that of increased resistance to fungal pathogens".

Applicants have removed recitation to "fragment" and "at least 15 consecutive nucleotides of SEQ ID NO:15" in claims 1 and 4.

Applicants respectfully submit that support for interpretation of term "knockout" is to be found in the specification at page 6, lines 14-15; page 36, lines 11-24; and in prior application 60/197,899 filed April 17, 2000, incorporated by reference in its entirety, in which the experimental protocol for producing the G896 polynucleotide "knockout" plant is described (copy of filing receipt and Application Cover Sheet enclosed as Exhibit 3). As shown in a copy of the experimental protocol as originally filed in the above referenced Provisional Patent Application, the G896 "knockout" mutant contains a T-DNA insertion 40 base pairs downstream of the start codon. (Copies of pages in Appendix from application 60/197,899 which disclose G896 (SEQ ID NOs:15 and 110) herewith submitted as "Appendix A")

Applicants further respectfully submit that support for the unique identifying features of the polynucleotide of SEQ ID NO:15 is to be found in the specification in Figure 1 at SEQ ID NO:15, third column, where the polypeptide coding sequence co-ordinates 47-1150 are disclosed, as described in the specification at page 4, lines 4-8. Figure 1, at SEQ ID NO:15, also discloses the conserved domain of the encoded polypeptide, at amino acid coordinates 18-39. Applicants have submitted a substitute "Sequence Listing" which discloses the polypeptide sequence SEQ ID NO:110, which is the polypeptide sequence encoded by SEQ ID NO:15. SEQ ID NO:110 was disclosed as the polypeptide encoded by SEQ ID NO:15 in US Provisional Application Ser. No. 60/197,899, from which the instant application claims priority in part. Applicants respectfully draw the Examiner's attention to the copy of the Filing Receipt of the Provisional Application, as mailed by the PTO on 06/21/2000, as well as Applicants' Cover Sheet, mailed with the Provisional Application on 04/17/2000. The Cover Sheet shows that Applicants included "Appendix" in the filing papers; Applicants submit that the "Appendix" included three pages relating to SEQ ID NO:15 and SEQ ID NO:110 (G896) which disclosed the "knock-out" phenotype, polynucleotide sequence and encoded polypeptide sequence, as well as other polynucleotide and polypeptide homologs identified using BLASTX, copies herewith submitted as "Appendix A".

Figure 2 of the instant application, at SEQ ID NO:15, discloses at columns three and four that when the polynucleotide was experimentally "knocked-out" (KO) in an experimental plant, the resulting plant was more susceptible to *Fusarium* infection. Applicants respectfully submit that one of skill in the art would have a reasonable expectation that a transgenic plant over-expressing SEQ ID NO:15 (G896) would have increased tolerance to infection by *Fusarium*.

Applicants respectfully submit that Applicants disclosed in the specification at page 13, lines 4-19, continued on page 14, lines 1-22, and Table 1, the scope of silent and conservative substitutions in the polynucleotide of the invention.

With the arguments and rebuttals set forth above, together with the amendment of claims 1, 4, and 13, Applicants respectfully request that the rejection of claims 1-8, 13, 14, and 25 under 35 U.S.C. § 112, first paragraph, be withdrawn.

Rejection of Claims 1-8, 13, 14, 25, and 26 under 35 U.S.C. § 102

17. The Examiner rejected claims 1-8, 13, 14, 25, and 26 under 35 U.S.C. § 102(e) as being anticipated by Thomashow *et al* (U.S. Patent 6,417,428, filed 23 November 1998).

The Examiner stated that the limitation at claims 1(e) and 4(e) "hybridizes under stringent conditions" has been found to be indefinite as discussed supra. In addition, the limitation at claims 1 (g) and 4(g) "or fragment encodes a polypeptide that modifies a plant's trait" has been interpreted to the broadest extent, and may encompass any fragment that encodes a polypeptide that modifies a plant's trait. the nucleotide sequence to which said claims is directed may encode a conservatively substituted variant as claimed in claims 1 (b) and 4(b). The Examiner stated that Thomashow discloses a transgenic plant with the modified trait of enhanced freezing tolerance, said transgenic plant having been transformed with an expression vector comprising a constitutive promoter operably linked to a polynucleotide comprising a nucleotide sequence comprising a fragment of Applicant's SEQ ID NO: 15 that encodes a polypeptide that modifies a plant's trait, that being the *Arabidopsis thaliana* transcription factor CBF1, SEQ ID NO: 12, for example (see claims 9 and 28). The Examiner stated that said transgenic plant over-expresses the CBF1 transcription factor and alters the transgenic *Arabidopsis* plant's tolerance to freezing. The Examiner stated that Thomashow also discloses a method of producing a plant having a modified characteristic (see claim 11). Hence, the Examiner concluded, Thomashow has previously disclosed all of the claim limitations.

18. The Examiner rejected claim 4 under 35 U.S.C. § 102(b) as anticipated by Newman *et al.* 1994 (Plant Physiology 106:1241-1255) taken with the evidence of Newman 1998 (Genbank Accession Number H76651, submitted 5 January 1998).

The Examiner stated that Newman discloses an isolated polynucleotide comprising a nucleotide sequence comprising at least 15 consecutive nucleotide of SEQ ID NO: 15. said polynucleotide would hybridize under "stringent conditions" to a polynucleotide having the nucleotide sequence of SEQ ID NO:

15 (see Genbank Accession Number H76651). The Examiner stated that the polynucleotide of Newman from base-pair 30-427 is 92.7% similar to Applicant's SEQ ID NO: 15 from base-pair 1-398.

In response, Applicants have amended claim 1 to recite: "A transgenic plant comprising a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:110; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of SEQ ID NO:110; (c) a nucleotide sequence comprising SEQ ID NO:15; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and (f) a nucleotide sequence comprising the complementary nucleotide sequence of a nucleotide sequence of (a), (b), (c), (d), or (e)".

Applicants have amended claim 4 to recite: "An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO:110; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of SEQ ID NO:110; (c) a nucleotide sequence comprising SEQ ID NO:15; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and (f) a nucleotide sequence comprising the complementary nucleotide sequence of a nucleotide sequence of (a), (b), (c), (d), or (e)".

Applicants' arguments regarding the validity of reciting time limits as parameters for stringent hybridization conditions are discussed *supra*. Applicants have removed recitation to "fragment" and "at least 15 consecutive nucleotides of SEQ ID NO:15" in claims 1 and 4.

Applicants have canceled claim 26. Therefore, with the amendments to claims 1 and 4 set forth above, Applicants respectfully request that the rejection of claims 1-8, 13, 14, and 25 under 35 U.S.C. § 102 (e) and of claim 4 under 35 U.S.C. § 102 (b), be withdrawn.

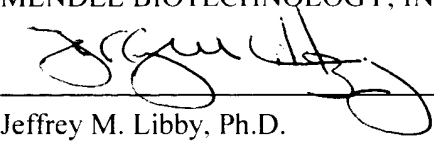
CONCLUSION

Applicants have requested a two (2) month extension of time to respond to the Examiner's instant Office Action. Applicants believe that no additional fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Mendel

Biotechnology, Inc. Deposit Account No. 501025. This form is enclosed in duplicate.

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.

Date: Dec 27, 2002



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VERSION TO SHOW CHANGES MADE
IN THE SPECIFICATION

Please replace at page 1, lines 4-6 with the following paragraph:

-- The present invention claims the benefit from US Provisional Patent Application Serial Nos. 60/166,228 filed November 17, 1999 and 60/197,899 filed April 17, 2000 and ["Plant Trait Modification III"] 60/227,439 filed August 22, 2000. --

Please replace at page 31, line 1, with the following:

-- through the National Center for Biotechnology Information ([<http://www.ncbi.nlm.nih.gov/>] [ncbi.nlm.nih](http://www.ncbi.nlm.nih.gov/); see at world wide web (www) National Institutes of Health US Government (gov) website).
 This --

Please replace the first paragraph of page 19 of the specification with the following paragraph:

-- *Biol.* 26:1947-1959), carpels (Ohl et al. (1990) *Plant Cell* 2:837-848), pollen and ovules (Baerson et al. (1993) *Plant Mol. Biol.* 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al (1999) *Plant Mol. Biol.* 39:979-990 or Baumann et al. (1999) *Plant Cell* 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) *Plant Mol. Biol.* 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) *Plant Mol. Biol.* 38:1053-1060, Willmott et al. (1998) *Plant Mol. Biol.* 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley, et al. (1993) *Plant Mol. Biol.* 22: 13-23), light (e.g., the pea *rbcS*-3A promoter, Kuhlemeier et al., (1989) *Plant Cell* 1:471-478, and the maize *rbcS* promoter, Schaffner and Sheen, (1991) *Plant Cell* 3: 997-1012); wounding (e.g., *wun1*, Siebertz et al., (1989) *Plant Cell* 1: 961-968); pathogen resistance, and chemicals such as methyl jasminate or salicylic acid (Gatz et al., (1997) *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (Gan and Amasino [An and Amazon] (1995) *Science* 270: 1986-1988); or late seed development (Odell et al. (1994) *Plant Physiol.* 106:447-458). --

IN THE CLAIMS

Please amend claims 1, 4, 13, 14, 25, and 27 as follows:

1. (Amended) A transgenic plant [with a modified trait, which plant comprises] comprising a

recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising [a sequence selected from a sequence in Appendix A] SEQ ID NO:110 [, or a complementary nucleotide sequence thereof];
- (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of [a] the polypeptide of [(a)] SEQ ID NO:110 ;
- (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID [Nos. N-1, where N=1-109 or Appendix A] NO:15 [, or a complementary nucleotide sequence thereof];
- (d) a nucleotide sequence comprising silent substitutions in [a] the nucleotide sequence of (c);
- (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and
- (f) a nucleotide sequence comprising [at least 15 consecutive nucleotides of] the complementary nucleotide sequence of a nucleotide sequence of [any of (a)-(e)] (a), (b), (c), (d), or (e) [;
- (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's trait;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
- (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of Appendix A;
- (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of Appendix A; and
- (l) a nucleotide sequence which encodes a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A].

4. (Amended) An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising [a sequence selected from a sequence in Appendix A] SEQ ID NO:110 [, or a complementary nucleotide sequence thereof];
- (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of [a] the polypeptide of [(a)] SEQ ID NO:110 ;
- (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID [Nos. N-1, where N=1-109 or Appendix A] NO:15 [, or a complementary nucleotide sequence thereof];

- (d) a nucleotide sequence comprising silent substitutions in [a] the nucleotide sequence of (c);
- (e) a nucleotide sequence which hybridizes under stringent conditions to a polynucleotide comprising a nucleotide sequence of one or more of: (a), (b), (c), or (d); and
- (f) a nucleotide sequence comprising [at least 15 consecutive nucleotides of] the complementary nucleotide sequence of a nucleotide sequence of [any of (a)-(e)] (a), (b), (c), (d), or (e) [;
- (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's trait;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);
- (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of Appendix A;
- (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of Appendix A; and
- (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of Appendix A].

13. (Amended) A method for producing a modified plant having a modified [characteristic] trait , the method comprising : (i) transforming a plant with [altering the expression of] the isolated or recombinant polynucleotide of claim 4 [or the expression levels or activity of a polypeptide of claim 6 in a plant], thereby producing a modified plant[,] and (ii) selecting the modified plant for a modified trait thereby providing the modified plant with a modified trait, wherein the trait so modified is that of increased resistance to fungal pathogens.

14. (Amended) The method of claim 13 wherein the polynucleotide is [a] the polynucleotide of claim 4.

25. (Amended) A plant comprising altered expression levels of [an] the isolated or recombinant polynucleotide of claim 4.

27. (Amended) A plant lacking a nucleotide sequence [encoding a] of the polynucleotide of claim [11] 4 .